

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/560,299
Source: IFWP
Date Processed by STIC: 12/20/05

ENTERED



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/560,299

DATE: 12/20/2005

TIME: 11:26:24

Input Set : A:\08321-110PC2 SEQLIST.txt

Output Set: N:\CRF4\12202005\J560299.raw

4 <110> APPLICANT: Thomas Jefferson University
 7 <120> TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS
 8 AND METHODS FOR MAKING AND USING THE SAME
 11 <130> FILE REFERENCE: 08321-110PC2
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/560,299
 C--> 13 <141> CURRENT FILING DATE: 2005-12-12
 13 <150> PRIOR APPLICATION NUMBER: US 10/461,148
 14 <151> PRIOR FILING DATE: 2003-06-13
 17 <160> NUMBER OF SEQ ID NOS: 24
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 474
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Human
 26 <400> SEQUENCE: 1
 27 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
 28 1 5 10 15
 29 Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 30 20 25 30
 31 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 32 35 40 45
 33 Ser Asn Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 34 50 55 60
 35 Glu Trp Val Ser Ala Ile Ser Ala Ser Gly His Ser Thr Tyr Leu Ala
 36 65 70 75 80
 37 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 38 85 90 95
 39 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 40 100 105 110
 41 Tyr Tyr Cys Ala Lys Asp Arg Glu Val Thr Met Ile Val Val Leu Asn
 42 115 120 125
 43 Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Arg Val Thr Val Ser Ser
 44 130 135 140
 45 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 46 145 150 155 160
 47 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 48 165 170 175
 49 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 50 180 185 190
 51 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 52 195 200 205
 53 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 54 210 215 220

p.6

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```

55 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
56 225                230                235                240
57 Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
58                245                250                255
59 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
60                260                265                270
61 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
62                275                280                285
63 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
64                290                295                300
65 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
66 305                310                315                320
67 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
68                325                330                335
69 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
70                340                345                350
71 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
72                355                360                365
73 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
74                370                375                380
75 Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
76 385                390                395                400
77 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
78                405                410                415
79 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
80                420                425                430
81 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
82                435                440                445
83 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
84                450                455                460
85 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
86 465                470
89 <210> SEQ ID NO: 2
90 <211> LENGTH: 234
91 <212> TYPE: PRT
92 <213> ORGANISM: Human
94 <400> SEQUENCE: 2
95 Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
96 1                5                10                15
97 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
98                20                25                30
99 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ala Cys Arg Ala Ser Gln Thr
100                35                40                45
101 Ala Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
102                50                55                60
103 Arg Leu Leu Ile Tyr Asp Thr Ser Asn Arg Ala Thr Gly Ile Pro Ala
104 65                70                75                80
105 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser
106                85                90                95

```

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```

107 Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Phe
108           100           105           110
109 Asn Trp Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Phe Lys Arg
110           115           120           125
111 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
112           130           135           140
113 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
114 145           150           155           160
115 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
116           165           170           175
117 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
118           180           185           190
119 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
120           195           200           205
121 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
122           210           215           220
123 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
124 225           230
127 <210> SEQ ID NO: 3
128 <211> LENGTH: 1557
129 <212> TYPE: DNA
130 <213> ORGANISM: Human
132 <400> SEQUENCE: 3
133 atggacacac tttgctccac gctcctgctg ctgaccatcc cttcatgggt cttgtcccaa 60
134 attaccttga aggagactgg tcctacgctg gtgaaaccca cacagaccct cacgctgacc 120
135 tgcaccttct cggggttctc actcagcact agtggagtgg gtgtgggctg gatccgtcag 180
136 cccccaggaa aggccctgga gtgggttaca ctcatattatt gggatgatga taagcgttac 240
137 agtccatctc tggagaacag ggtcaccatc aggaaggaca cctccaaaaa ccagggtggct 300
138 cttacaatga cgaacatgga ccctttggac acaggcacat actactgtgc gcacagacaa 360
139 catatcagca gcttcccgtg gttecgattc tggggccagg gaaccctggg caccgtctcc 420
140 tcagcttcca ccaagggccc atcggtcttc cccctggcgc cctgctccag gagcacctct 480
141 gggggcacag cggccctggg ctgctgtgtc aaggactact tccccgagcc ggtgacgggtg 540
142 tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 600
143 tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcacccag 660
144 acctacacct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag 720
145 ctcaaaaccc cacttggtga cacaactcac acatgcccac ggtgcccaga gcccaaactct 780
146 tgtgacacac ctccccctg cccacgggtg ccagagccca aatcttgtga cacacctccc 840
147 cegtgcccac ggtgcccaga gcccaaactct tgtgacacac ctcccccatg cccacgggtg 900
148 ccagcacctg aactcctggg aggaccgtca gtcttctct tccccccaaa acccaaggat 960
149 acccttatga tttcccggac ccctgaggtc acgtgcgtgg tgggtggacgt gagccacgaa 1020
150 gaccccagag tccagttaa gtggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1080
151 aagccgcggg aggagcagtt caacagcacg ttccgtgtgg tcagcgtcct caccgtcctg 1140
152 caccaggact ggctgaacgg taaggagtac aagtgaagg tctccaacaa agccctccca 1200
153 gcccccatcg agaaaacat ctccaaaacc aaaggacagc cccgagaacc acagggtgtac 1260
154 accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctgggtc 1320
155 aaaggcttct accccagcga catcgccgtg gagtgggaga gcagcgggca gccggagaac 1380
156 aactacaaca ccacgcctcc catgctggac tccgacggct ccttcttct ctacagcaag 1440
157 ctacccgtgg acaagagcag gtggcagcag gggaacatct tctcatgctc cgtgatgcat 1500
158 gaggtctctg acaaccgctt cacgcagaag agcctctccc tgtctccggg taaatga 1557

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```

160 <210> SEQ ID NO: 4
161 <211> LENGTH: 518
162 <212> TYPE: PRT
163 <213> ORGANISM: Human
165 <400> SEQUENCE: 4
166 Met Asp Thr Leu Cys Ser Thr Leu Leu Leu Leu Thr Ile Pro Ser Trp
167 1 5 10 15
168 Val Leu Ser Gln Ile Thr Leu Lys Glu Thr Gly Pro Thr Leu Val Lys
169 20 25 30
170 Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
171 35 40 45
172 Ser Thr Ser Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
173 50 55 60
174 Ala Leu Glu Trp Val Thr Leu Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
175 65 70 75 80
176 Ser Pro Ser Leu Glu Asn Arg Val Thr Ile Arg Lys Asp Thr Ser Lys
177 85 90 95
178 Asn Gln Val Ala Leu Thr Met Thr Asn Met Asp Pro Leu Asp Thr Gly
179 100 105 110
180 Thr Tyr Tyr Cys Ala His Arg Gln His Ile Ser Ser Phe Pro Trp Phe
181 115 120 125
182 Asp Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
183 130 135 140
184 Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
185 145 150 155 160
186 Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
187 165 170 175
188 Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
189 180 185 190
190 Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
191 195 200 205
192 Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys
193 210 215 220
194 Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
195 225 230 235 240
196 Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro
197 245 250 255
198 Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu
199 260 265 270
200 Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro
201 275 280 285
202 Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu
203 290 295 300
204 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
205 305 310 315 320
206 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
207 325 330 335
208 Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr Val Asp Gly
209 340 345 350

```

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```

210 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
211          355          360          365
212 Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
213      370          375          380
214 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
215 385          390          395          400
216 Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
217          405          410          415
218 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
219          420          425          430
220 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
221          435          440          445
222 Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr
223      450          455          460
224 Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
225 465          470          475          480
226 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys
227          485          490          495
228 Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu
229          500          505          510
230 Ser Leu Ser Pro Gly Lys
231      515
234 <210> SEQ ID NO: 5
235 <211> LENGTH: 699
236 <212> TYPE: DNA
237 <213> ORGANISM: Human
239 <400> SEQUENCE: 5
240 atggcctgga ccgttctcct cctcggcctc ctctctcact gcacagggtc tgtgacgtcc 60
241 tatgtgctga ctcagccacc ctcggtgtca gtggccccag gaaagacggc caggattaac 120
242 tgtgggggaa acaacattga atatagaagt gtgcactggg accagcagaa gtcaggccag 180
243 gcccctgtag cggatcatcta tgataatagt gaccggccct cagggatccc tgagcgattc 240
244 tctggttcca aatctgggaa cacggccacc ctgaccatca gcagggtcga agccggggat 300
245 gaggccgact attactgtca ggtgtgggat attagtagtg atgtggtctt cggcggaggg 360
246 accaagctga ccgtcctagg tcagcccaag gctgccccct cggtcactct gttcccggcc 420
247 tcctctgagg agcttcaagc caacaaggcc acactgggtg gtctcataag tgacttctac 480
248 ccgggagccg tgacagtggc ctggaaggca gatagcagcc ccgtcaaggc gggagtggag 540
249 accaccacac cctccaaaca aagcaacaac aagtacgcgg ccagcagcta tctgagcctg 600
250 acgcctgagc agtggaaagc ccacagaagc tacagctgcc aggtcacgca tgaagggagc 660
251 accgtggaga agacagtggc ccctacagaa tgttcatag 699
253 <210> SEQ ID NO: 6
254 <211> LENGTH: 232
255 <212> TYPE: PRT
256 <213> ORGANISM: Human
258 <400> SEQUENCE: 6
259 Met Ala Trp Thr Val Leu Leu Leu Gly Leu Leu Ser His Cys Thr Gly
260 1          5          10          15
261 Ser Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala
262      20          25          30
263 Pro Gly Lys Thr Ala Arg Ile Asn Cys Gly Gly Asn Asn Ile Glu Tyr

```

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; N Pos. 37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56

VERIFICATION SUMMARY

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Input Set : A:\08321-110PC2 SEQLIST.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:552 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:556 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:557 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0